



Protein families database of alignments and HMMs

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UBA



Figure 1: 1aip
C complex of two elongation factors
 Ef-tu ef-ts complex from thermus thermophilus

Key:

D main	Chain	Start Residue	End Residue
GTP_EFTU_D3	A	309	404
GTP_EFTU_D2	A	235	305
GTP_EFTU	A	9	214
GTP_EFTU_D3	B	309	404
GTP_EFTU_D2	B	235	305
GTP_EFTU	B	9	214
UBA	C	2	42
EF_TS	C	55	196
UBA	D	2	42
EF_TS	D	55	196
GTP_EFTU_D3	E	309	404
GTP_EFTU_D2	E	235	305
GTP_EFTU	E	9	214
GTP_EFTU_D3	F	309	404
GTP_EFTU_D2	F	235	305
GTP_EFTU	F	9	214
UBA	G	2	42
EF_TS	G	55	196
UBA	H	3	42
EF_TS	H	55	196

The Swissprot/PDB mapping was provided by [MSD](#)

Accession number: PF00627

UBA/TS-N domain

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This small domain is composed of three alpha helices. This family includes the previously defined UBA and TS-N domains. The UBA-domain (ubiquitin associated domain) is a novel sequence motif found in several proteins having connections to ubiquitin and the ubiquitination pathway. The structure of the UBA domain consists of a compact three helix bundle [1]. This domain is found at the N terminus of EF-TS hence the name TS-N. The structure of EF-TS is known and this domain is implicated in its interaction with EF-TU [2]. The domain has been found in non EF-TS proteins such as alpha-NAC [P70670](#) and MJ0280 [Y280_METJA](#) [1].

This family forms **structural complexes** with other Pfam families, to view them click [here](#)

INTERPRO description (entry IPR000449)

UBA domains are a commonly occurring sequence motif of approximately 45 amino acid residues that are found in diverse proteins involved in the ubiquitin/proteasome pathway, DNA excision-repair, and cell signaling via protein kinases [[MEDLINE:97025177](#)]. The human homologue of yeast Rad23A is one example of a nucleotide excision-repair protein that contains both an internal and a C-terminal UBA domain.

The solution structure of human Rad23A UBA(2) showed that the domain forms a compact three-helix bundle [[MEDLINE:99061330](#)]. Comparison of the structures of UBA(1) and UBA(2) reveals that both form very similar folds and have a conserved large hydrophobic surface patch which may be a common protein-interacting surface present in diverse UBA domains. Evidence that ubiquitin binds to UBA domains leads to the prediction that the hydrophobic surface patch of UBA domains interacts with the hydrophobic surface on the five-stranded β -sheet of ubiquitin [[MEDLINE:22075341](#)].

1dv0 ▾	Display pdb
For additional annotation, see the PROSITE document PDOC50015 [Expasy SRS-UK SRS-USA]	

Alignment	Domain organisation
<input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528) Format Coloured alignment ▾ <div> Get alignment View HMM logo </div> Further alignment options here Help relating to Pfam alignments here	<input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528) <input type="radio"/> Context (58) <div> <div> As a Graphic Zoom 0.5 pixels/aa. <input type="checkbox"/> Bootstrap tree View Graphic </div> <div> As a Tree NIFAS Applet </div> </div> To find out about the NIFAS tree-viewer, click here
Species Distribution	Phylogenetic tree
NEW! View alignments & domain organisation by species Tree depth: Show all levels ▾ View Species Tree	<input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528) <div> Download tree ATV Applet </div> The trees were generated using Quicktree To find out more about ATV phylogenetic tree-viewer click here

Database References	
PDB You can find out how to set up Rasmol here	<div>1dv0 A; 1; 40; ▾</div> <div> PDB; 2 Pfam Scop Cath Pfam </div> <div> CATH-PDBSUM SCOP-UK </div>
PROSITE	PDOC50015 [Expasy SRS-UK SRS-USA]
URL	http://www.isrec.isb-sib.ch/profile/isrec96/poster.html
PROSITE_PROFILE	PS50030
HOMSTRAD	EF_TS
PFAMB	PB009949 PB014089 PB027029 PB047420 PB054475 PB092955 PB0940
SYSTERS	UBA
PANDIT	UBA

Literature References	Pfam specific information	
1. The structure of the <i>Escherichia coli</i> EF-Tu.EF-Ts complex at 2.5 Å resolution. Kawashima T, Berthet-Colominas C, Wulff M, Cusack S, Leberman R; <i>Nature</i> 1996;379:511-518.	Author of entry	Bateman A
	Type definition	Domain
	Alignment method of seed	Manual
	Source of seed members	Bateman A

2.

Structure of a human DNA repair protein UBA domain that interacts with HIV-1 Vpr.

Dieckmann T, Withers-Ward ES, Jarosinski MA, Liu CF, Chen IS, Feigon J;
Nat Struct Biol 1998;5:1042-1047.

3. Alignment of TS-N domain is in figure 7c.

Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell.

Makarova KS, Aravind L, Galperin MY, Grishin NV, Tatusov RL, Wolf YI, Koonin EV;
Genome Res 1999;9:608-628.

HMMER build information

	Pfam_ls [Download HMM]	Pfam_fs [Download HMM]
Gathering cutoff	17.3 17.3;	19.0 19.0
Trusted cutoff	17.3 17.3;	19.0 19.0
Noise cutoff	17.2 17.2;	18.9 18.9
Build method of HMM	hmmbuild -F HMM_ls SEED hmmcalibrate --seed 0 HMM_ls	hmmbuild -f -F HMM_fs SEED hmmcalibrate --seed 0 HMM_fs

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